

Accuracy Estimation of Biometrics Systems: *The Subsets Bootstrap*

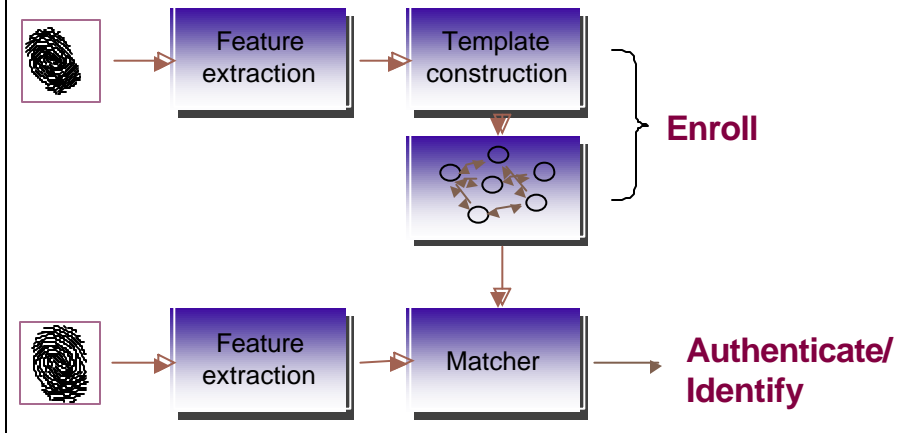
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Outline

- Biometrics systems
- Performance accuracy
- Probability densities and distributions
- The match score distribution
- Confidence interval
- The Bootstrap
- The Subsets Bootstrap
- Experiments
- Conclusions

Biometrics Systems



Pattern Recognition System

Two hypotheses:

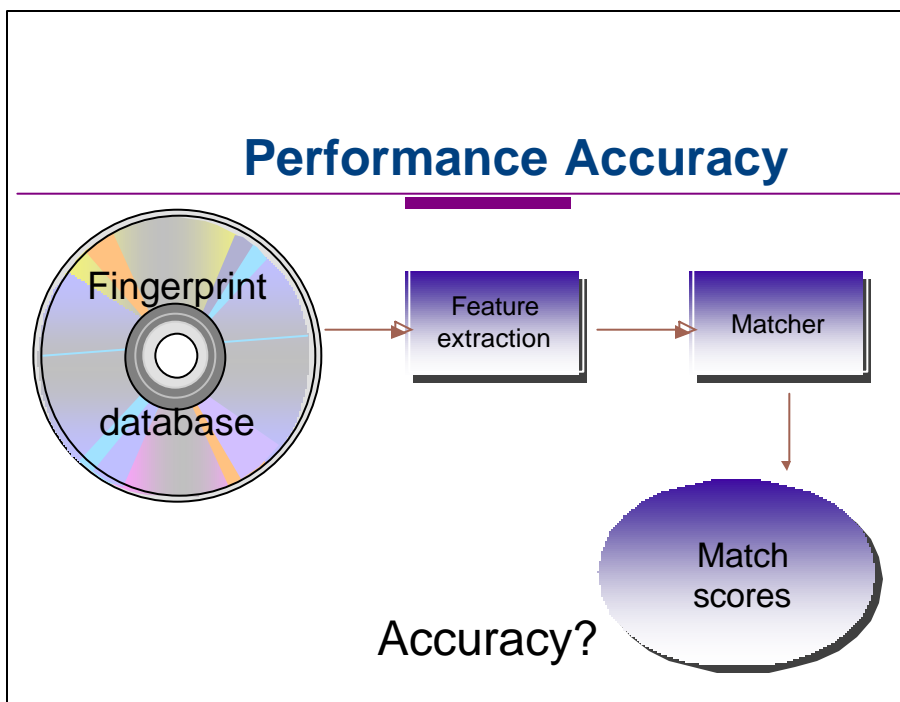
H_o : $b = b'$, the claimed identity is correct

H_1 : $b \neq b'$, the claimed identity is not correct

Two errors:

A False Reject: Decide H_1 while H_o is true

A False Accept: Decide H_o while H_1 is true



What is Accuracy?

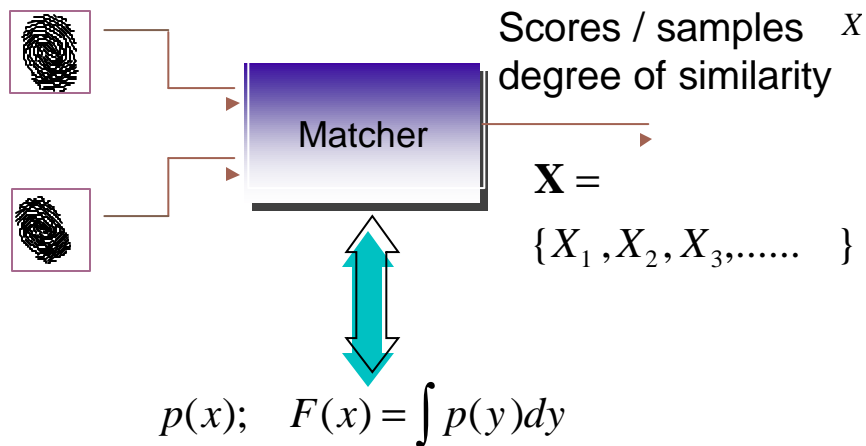
- False reject and false accept rates?
- Equal error rate?
- d-prime?
- Receiver Operator Characteristic curve (ROC)?

- All these are estimates....
- What is the significance of the estimator(s), i.e., confidence intervals?

Confidence Interval Estimation

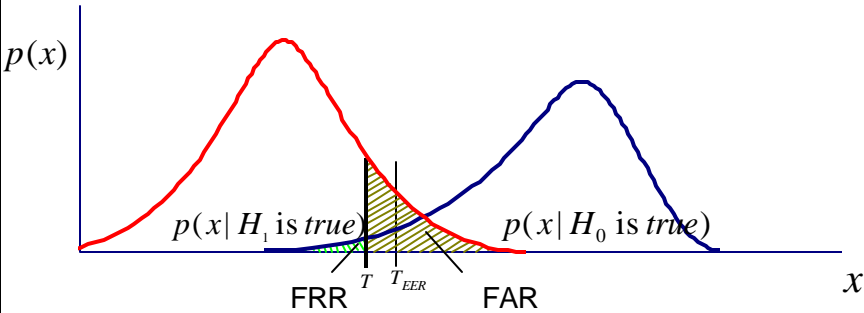
- **Parametric**
 - Assumes some parametric form of the underlying distribution
 - Binomial distribution of match scores; uses law of large numbers
- **Non-parametric**
 - Bootstrap
- **Both methods assume i.i.d. samples**
 - independently distributed
 - identically distributed

What is a Matcher?

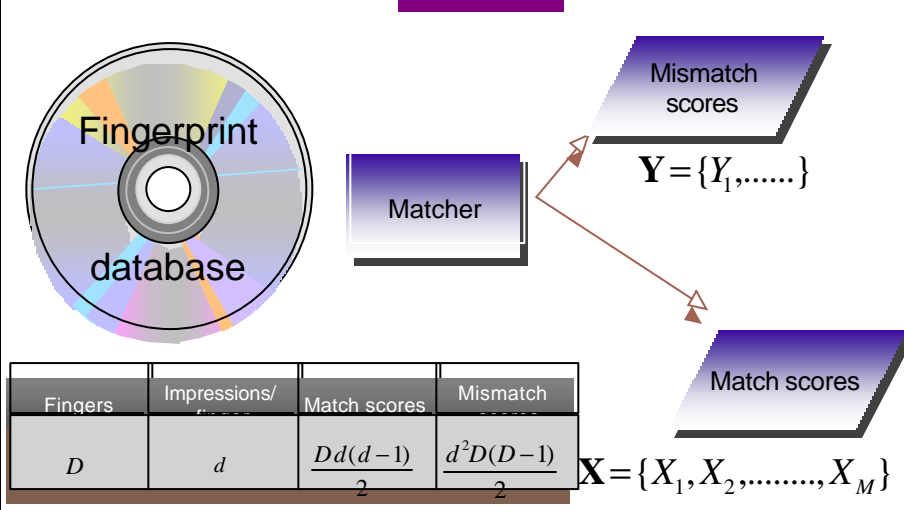


FARs and FRRs

- **Decide a match if:** $x \geq T$
- **Tradeoff between FRR and FAR**



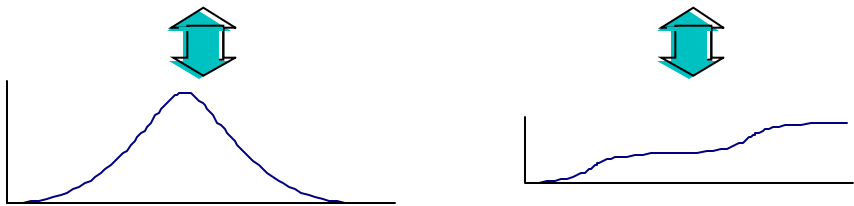
Generating Match Scores



Probability Density

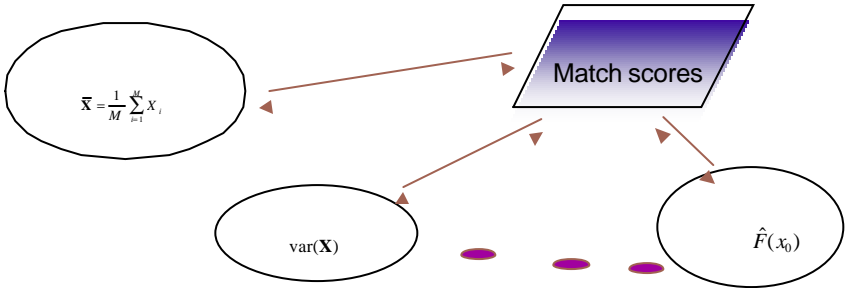
Of match scores $\mathbf{X} = \{X_1, X_2, \dots\}$

$p(x | H_0 = true)$ $F(x) = \int_{-\infty}^x p(y | H_0 = true) dy$



Computing Statistics

$\mathbf{X} = \{X_1, X_2, \dots\}$

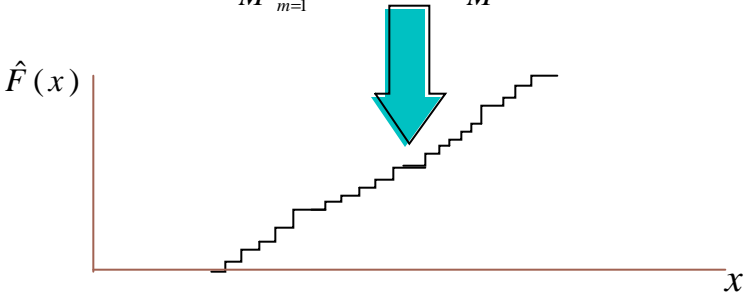


Any statistic of \mathbf{X} is only an estimate:
error measures are statistics, hence,
random variables

Empirical Distribution

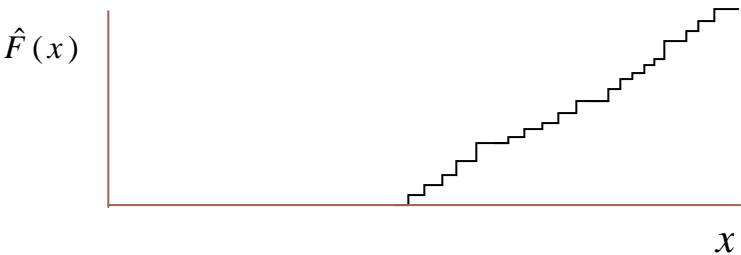
Match scores: $\mathbf{X} = \{X_1, X_2, \dots, X_M\}$

$$\hat{F}(x) = \frac{1}{M} \sum_{m=1}^M \mathbf{1}(X_m \leq x) = \frac{1}{M} \#(X_m \leq x)$$



The Bootstrap

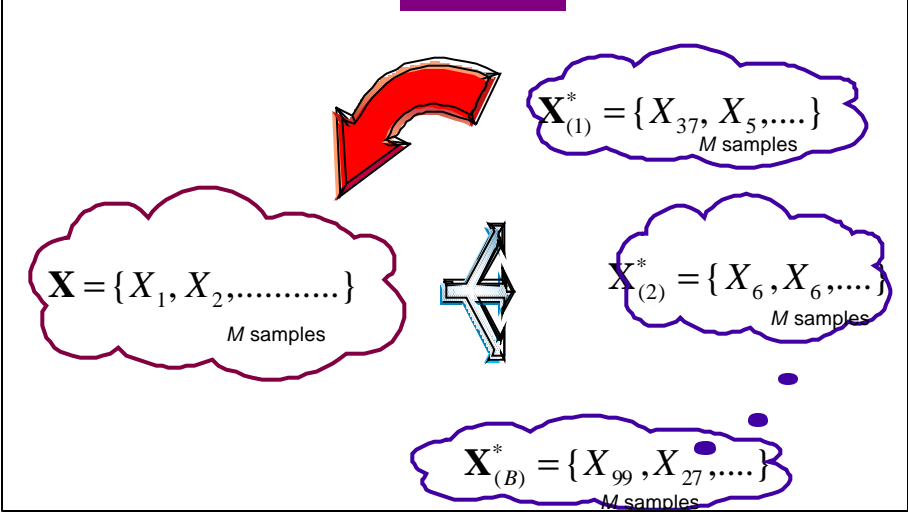
Assume $\hat{F}(x)$ is the true distribution $F(x)$



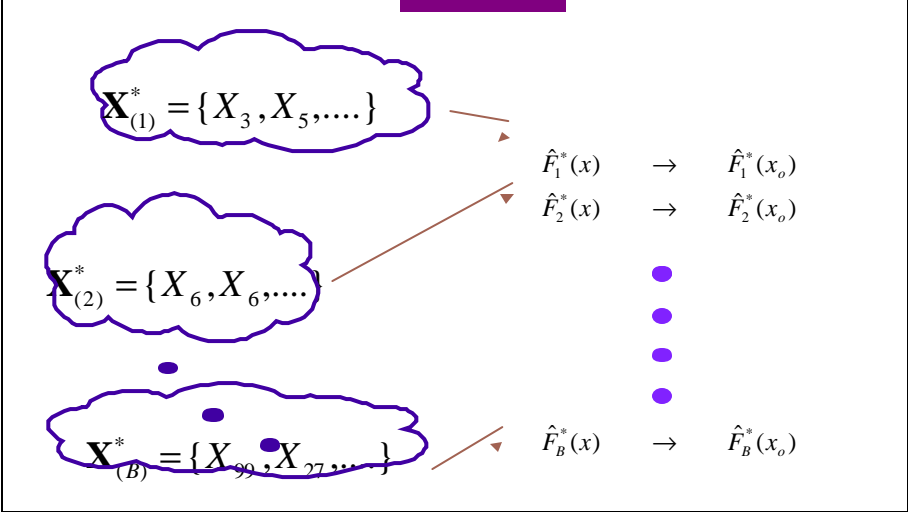
Sample \mathbf{X} many (B) times, with replacement

→ $\mathbf{X}_{(1)}^*, \mathbf{X}_{(1)}^*, \dots, \mathbf{X}_{(B)}^*$

Sampling with replacement



Bootstrap Estimates

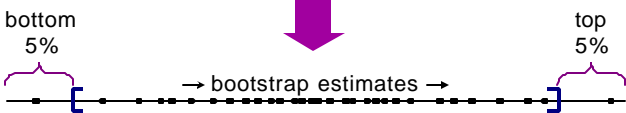


Ordering and Counting

$$\{\hat{F}_1^*(x_o), \hat{F}_2^*(x_o), \dots, \hat{F}_B^*(x_o)\}$$

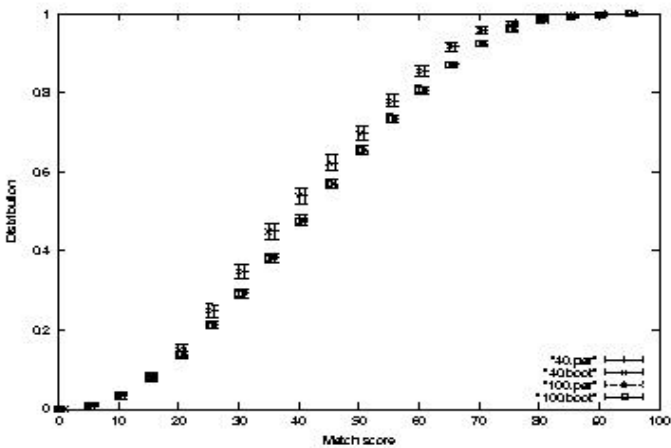


$$(\hat{F}_{(1)}^*(x_o) \leq \hat{F}_{(2)}^*(x_o) \leq \dots \leq \hat{F}_{(B)}^*(x_o))$$

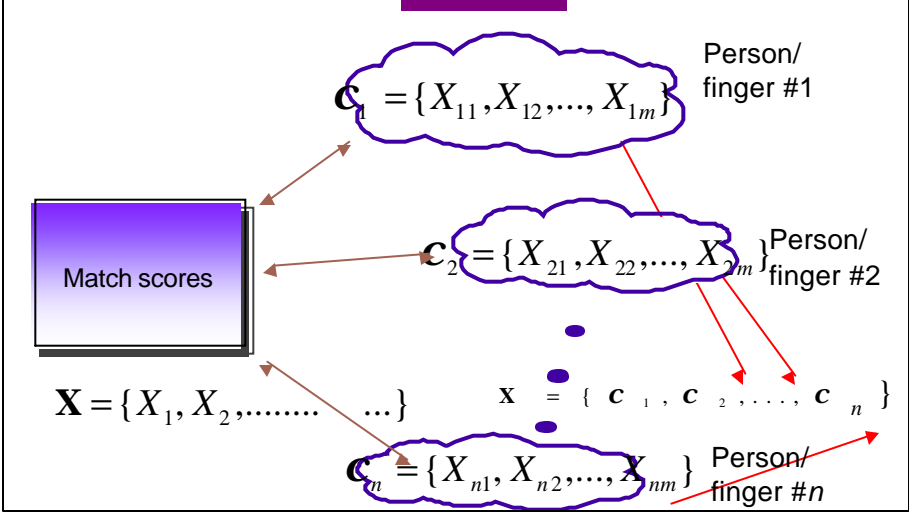


Confidence Intervals

False Reject Curve

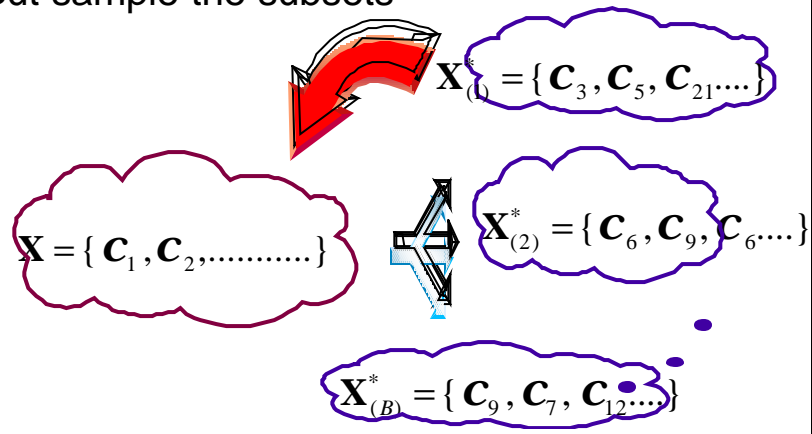


Match Scores not Independent

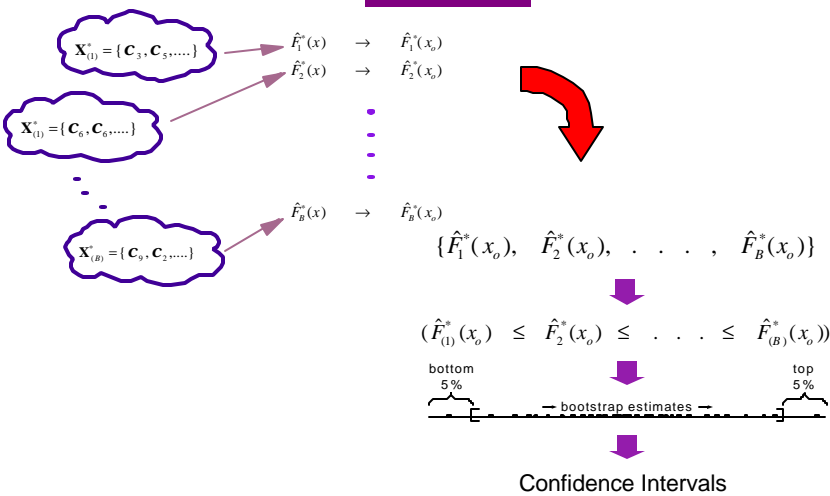


Sampling with Replacement

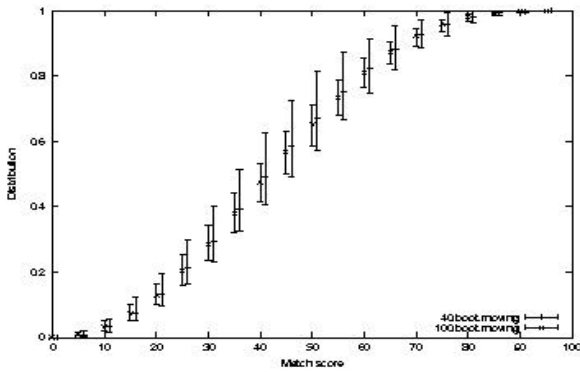
But sample the subsets



Estimates & Confidence Intervals



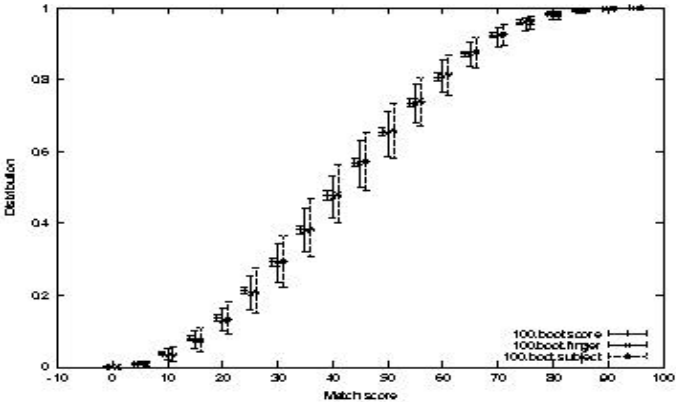
False Reject Rate Curve



Replication of Dependence

$$\begin{aligned} \mathbf{X} &= \{X_1, X_2, X_3, X_4, X_5, X_6, X_7, X_8, X_9, X_{10}, X_{11}, X_{12}, X_{13}, X_{14}, X_{15}, \dots, X_M\} \\ \mathbf{X}^* &= \{X_4, X_{11}, X_2, X_{15}, X_1, X_{12}, X_{11}, X_7, X_2, X_9, X_3, X_{13}, X_9, X_{13}, \dots, X_3\} \\ \mathbf{X} &= \{X_1^a, X_1^b, X_1^c, X_1^d, X_2^a, X_2^b, X_2^c, X_2^d, X_3^a, X_3^b, X_3^c, X_3^d, \dots, X_m^a, X_m^b, X_m^c, X_m^d\} \\ \mathbf{X} &= \{c_1, c_2, c_3, \dots, c_m\} \\ \mathbf{X}^* &= \{c_1, c_1, c_2, \dots, c_9\} \\ \mathbf{X}^* &= \{X_1^a, X_1^b, X_1^c, X_1^d, X_1^a, X_1^b, X_1^c, X_1^d, X_2^a, X_2^b, X_2^c, X_2^d, \dots, X_9^a, X_9^b, X_9^c, X_9^d\} \end{aligned}$$

Confidence Intervals



Conclusions

- Many methods for computing confidence intervals underestimate the intervals
- Parametric methods underestimate the variance when data are dependent
- This is also true for the traditional Bootstrap
- For any biometrics, samples of the same person are *not* independent
- Bootstrap not so sensitive to "identical" assumption
- Introduced the Subsets Bootstrap: Divide the scores up into subsets that are independent
 - Sample the set of subsets with replacement to form bootstrap sets
 - Gives realistic estimates of confidence intervals

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<http://www.research.ibm.com/people/r/ratha/autoid.html>